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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2008; month=12; day=16; hr=16; min=7; sec=8; ms=611;]
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Validated By CRFValidator v 1.0.3

Application No: 10574922 Version No: 1.0

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Finished: 2008-12-01 17:01:18.282
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 670 ms
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Total Errors: 0
No. of SeqIDs Defined: 19
Actual SeqID Count: 19

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<120> METHOD

<130> 092633-0104

<140> 10574922
<141> 2008-12-01

<150> PCT/US04/033391
<151> 2004-10-12

<150> 60/567,771
<151> 2004-05-05

<150> 60/526,571
<151> 2003-12-04

<150> 60/510,086
<151> 2003-10-10

<160> 19

<170> PatentIn Ver. 3.2

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<212> PRT
<213> Influenza A virus

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1 5 10 15

Gln Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys Leu Gly
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His His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr Asn Asp
35 40 45

Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser Ser
50 55 60

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<211> 65
<212> PRT
<213> Influenza A virus

<400> 2
Met Ala Ser Lys Thr Ile Ile Ala Leu Ser Tyr Ile Leu Cys Leu Val
1 5 10 15

Phe Ala Gln Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys
20 25 30

Leu Gly His His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr
35 40 45

Asn Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser
50 55 60

Ser
65

<210> 3
<211> 62
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
consensus sequence

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1 5 10 15

Lys Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys Leu Gly His
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His Ala Val Ser Asn Gly Thr Leu Val Lys Thr Ile Thr Asn Asp Gln
35 40 45

Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln Ser Ser Ser
50 55 60

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<211> 3759
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide vector sequence

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agccgtttct gtaatgaagg agaaaactca ccgaggcagt tccataggat ggcaagatcc 180
tggtatcggt ctgcgattcc gactcgtcca acatcaatac aacctattaa tttcccctcg 240
tcaaaaataa ggttatcaag tgagaaatca ccatgagtga cgactgaatc cggtgagaat 300
ggcaaaagct tatgcatttc tttccagact tgttcaacag gccagccatt acgctcgtca 360
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<211> 1503
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

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cttgaacggt ttgccgtgaa cccaggcctg ctggaaacat ctgagggatg tcgccagatc 180
ctggggcaat tgcagccatc cctccagacc gggagtgaag agctgaggtc cttgtataac 240
acagtggcta ccctctactg cgtacaccag aggatcgaga ttaaggatac caaggaggcc 300
ttggacaaaa ttgaggagga gcaaaacaag agcaagaaga aggcccagca ggcagctgct 360
gacactgggc atagcaacca ggtatcacag aactatccta ttgtccaaaa cattcagggc 420
cagatggttc atcaggccat cagcccccgg acgctcaatg cctgggtgaa ggttgtcgaa 480
gagaaggcct tttctcctga ggttatcccc atgttctccg ctttgagtga gggggccact 540
cctcaggacc tcaatacaat gcttaatacc gtgggcggcc atcaggccgc catgcaaatg 600
ttgaaggaga ctatcaacga ggaggcagcc gagtgggaca gagtgcatcc cgtccacgct 660
ggcccaatcg cgcccggaca gatgcgggag cctcgcggct ctgacattgc cggcaccacc 720
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gaatccttca ggtccggagt ggagaccaca acgcctcccc aaaaacagga accaatcgac 1440
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taa 1503

<210> 6
<211> 500
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
protein construct

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

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Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
                 85                  90                  95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
            100                 105                 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
        115                 120                 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
    130                 135                 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145                 150                 155                 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
                165                 170                 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
            180                 185                 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
        195                 200                 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
    210                 215                 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225                 230                 235                 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
                245                 250                 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
            260                 265                 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
        275                 280                 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
    290                 295                 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305                 310                 315                 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
                325                 330                 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
            340                 345                 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
        355                 360                 365

Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
    370                 375                 380
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Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
385                 390                 395                 400

Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
                405                 410                 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
            420                 425                 430

Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe
        435                 440                 445

Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
    450                 455                 460

Ser Gly Val Glu Thr Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp
465                 470                 475                 480

Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp
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Pro Ser Ser Gln
            500
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<210> 7
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

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ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180
ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240
acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300
ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360
gacacaggac acagcaatca ggtcagccaa aattacccta tagtgcagaa catccagggg 420
caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480
gagaaggctt tcagcccaga agtgataccc atgttttcag cattatcaga aggagccacc 540
ccacaagatt taaacaccat gctaaacaca gtgggggggac atcaagcagc catgcaaatg 600
ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtgcatcc agtgcatgca 660
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<210> 8
<211> 504
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
protein construct

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1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala

210 215 220